Observational cohort study of the clinical outcomes associated with B.1.1.7/SGTF among hospitalized COVID-19 patients in Lebanon

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Abstract

Background: The B.1.1.7 SARS-CoV-2 variant results in spike gene target failure (SGTF) in reverse transcription-quantitative polymerase chain reaction (RT-PCR) assays. Few studies have been published on the clinical impact of B.1.1.7/SGTF.

Aims: To assess the incidence of B.1.1.7/SGTF and its associated clinical characteristics among hospitalized COVID-19 patients.

Methods: This observational, single-centre, cohort study was conducted between December 2020 and February 2021 and included 387 hospitalized COVID-19 patients. The Kaplan–Meier method was used for survival analysis, and logistic regression to identify risk factors associated with B.1.1.7/SGTF.

Results: By February 2021, B.1.1.7/SGTF (88%) dominated the SARS-CoV-2 PCR results in a Lebanese hospital. Of the 387 eligible COVID-19 patients confirmed by SARS-CoV-2 RT-PCR, 154 (40%) were non-SGTF and 233 (60%) were B.1.1.1.7/SGTF; this was associated with a higher mortality rate among female patients [22/51 (43%) vs 7/37 (19%); $P = 0.0170$]. Among patients in the B.1.1.7/SGTF group, most were aged ≥ 65 years [162/233 (70%) vs 74/154 (48%); $P < 0.0001$]. Independent predictors of B.1.1.7/SGTF infection were hypertension (OR = 0.415; CI: 0.242–0.711; $P = 0.0010$), age ≥ 65 years (OR = 0.379; CI: 0.231–0.622; $P < 0.0001$), smoking (OR = 1.698; CI: 1.023–2.819; $P = 0.0410$), and cardiovascular disease (OR = 3.812; CI: 2.215–6.389; $P < 0.0001$). Only non-SGTF patients experienced multi-organ failure [5/154 (4%) vs 0/233 (0%); $P = 0.0096$].

Conclusion: There was a clear difference between the clinical features associated with B.1.1.7/SGTF and non-SGTF lineages. Tracking viral evolution and its clinical impact is crucial for proper understanding and management of the COVID-19 pandemic.

Keywords: COVID-19, in-hospital mortality, SARS-CoV-2, spike gene target failure, variant B.1.1.7

Citation: Dakroub F; Yassine M; Fakhredine S; Msheik A; Rahal H; Hayek G; et al. Observational cohort study of the clinical outcomes associated with B.1.1.7/SGTF among hospitalized COVID-19 patients in Lebanon. East Mediterr Health J. 2023;29(4):262–270. https://doi.org/10.26719/emhj.23.052

Received: 28/03/22; accepted: 08/12/22

Introduction

The highly pathogenic severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) emerged in Wuhan, China, and constituted a global public health emergency (*1*,*2*). Worldwide, reverse transcription-quantitative polymerase chain reaction (RT-PCR) is used to confirm the SARS-CoV-2 infection (*3*,*4*). At least 2 SARS-CoV-2 genes are targeted by the majority of the currently available RT-PCR assays. These include the 5′ frameshifted polyprotein (ORF1a/ORF1ab), nucleocapsid (N), envelope (E), spike (S) and RNA-dependent RNA polymerase (RdRP) genes (*5*). Multiplex PCR assays that detect several genes offer greater assay sensitivity (*6*).

The B.1.1.7 SARS-CoV-2 variant was reported on 14 December 2020 in the United Kingdom and is estimated to have emerged in September 2020 (*7*). It carries a deletion mutation at positions 69 and 70 in the spike protein that increases binding affinity to the angiotensin-converting enzyme 2 (ACE2) receptor (*8*). It results in S-gene target failure (SGTF) in some RT-PCR assays (*9*). The spike glycoprotein is an envelope protein that binds with high affinity to mammalian ACE2 (*10*).

Borges et al. suggested that SGTF or S gene target late detection (SGTL) can constitute a useful surrogate to track the spread of B.1.1.7 (*11*). Only a few studies have assessed the clinical impact of the B.1.1.7/SGTF (*12*–*14*), mostly in community settings (*15*–*18*). However, mortality can be more accurately investigated in a study of hospitalized patients. We aimed to assess the association of B.1.1.7/SGTF with clinical characteristics and outcomes of COVID-19 among hospitalized patients. We also aimed to trace the emergence and incidence of B.1.1.7/SGTF in a Lebanese hospital, adding evidence to the natural history of COVID-19. We then identified risk factors associated with the B.1.1.7/SGTF infection.

Methods

Study design

This was an observational, single-centre, prospective, cohort study involving 387 hospitalized COVID-19 patients admitted to Saint George Hospital, Beirut, Lebanon. The institutional review board at Al-Rassoul Hospital approved the study.

Participants and settings

Saint George Hospital is one of 2 Lebanese hospitals dedicated exclusively to treating COVID-19 cases in Lebanon. The cohort included adult COVID-19 patients admitted to the hospital between December 2020 and February 2021. The last included patient was admitted on 28 February 2021 and followed up until the final outcome was known. We excluded patients under 18 years of age, those discharged against medical advice, transferred to other hospitals, probable cases with a negative RT-PCR, and RT-PCR-confirmed cases without an S gene amplification result. Of 387 eligible patients, 154 were identified as non-SGTF and 233 as B.1.1.1.7/SGTF. Patients were followed up until death or hospital discharge after improvement.

Outcomes and variables

The COVID-19 diagnosis was confirmed by a positive RT-PCR result for SARS-CoV-2. The primary outcome was defined as in-hospital mortality associated with COVID-19 by direct cause or contribution. The main explanatory variable for this analysis was the spike gene detection status in the RT-PCR test. The covariates of interest included demographics, symptoms at admission and pre-existing comorbidities. Variables were used in their original scale, and age was categorized into groups aged ≥ 65 and < 65 years in the multivariate analysis. We chose this classification since the chronological age 65 or older typically defines the elderly. To adequately investigate its association with COVID-19 mortality, age was further classified into several groups.

The SARS-CoV-2 PCR test and definitions

The PCR tests were carried out in the laboratory department of Saint George Hospital for most of the patients included in the study. Nasopharyngeal swab specimens were collected for SARS-CoV-2 RNA extraction, which was carried out using the MagMAX Viral/Pathogen Kit II (Cat.# A48383, Thermofisher Scientific, Vilnius); RT-PCR was carried out using the TaqPath COVID-19 CE-IVD RT-PCR Kit (Cat.# A48067, Applied Biosystems, Bleiswijk), a triple target multiplex assay detecting the ORF1ab, N and S genes. The non-SGTF test result was defined as the positive amplification (Ct < 30) of the ORF1ab, N and S genes simultaneously in the PCR assay. We defined SGTF as the positive amplification (Ct < 30) of the ORF1ab and N genes, with an undetected S gene. We used SGTF as a proxy for lineage B.1.1.7 presence.

Data sources

Physicians extracted data from electronic patient records, including demographic and clinical characteristics, laboratory and pathology results, and disease outcomes. Cardiovascular disease (CVD) was defined as the presence of coronary artery syndrome, atrial fibrillation or heart failure. Acute respiratory distress syndrome was diagnosed according to the Berlin definition (*19*), and COVID-19 patients were stratified into mild, moderate, severe and critical based on COVID-19 guidelines in China (*20*). Septic shock was identified when sepsis-induced hypotension remained refractory to fluid resuscitation (*21*). Nosocomial infection was defined as an infectious disease acquired in Saint George Hospital at least 48 hours after admission. The occurrence of at least 2 dysfunctions of the pulmonary, renal and hepatic organs defined multi-organ failure.

To eliminate any potential source of bias during data collection, all hospitalized cases were enrolled between December 2020 and February 2021. Following data collection, a researcher independently eliminated ineligible cases according to the predetermined rigorous criteria. A priori study size calculation was not performed.

Statistical analyses

Analyses were carried out using *GraphPad* for Windows, version 8.4.3, and *SPSS*, version 25, was used for the multivariate analysis. Categorical variables were described as frequency and percentage and analysed using the chi-squared (χ^2) test and Fisher's exact test. Median and interquartile range (IQR) were used to report continuous variables, which were compared using the Mann–Whitney U-test or *t*-test. The Kolmogorov–Smirnov test was used to assess normality. Survival analysis was performed using the Kaplan–Meier method, and statistical differences in survival or intensive care unit (ICU) admission were assessed by the Gehan–Breslow–Wilcoxon test.

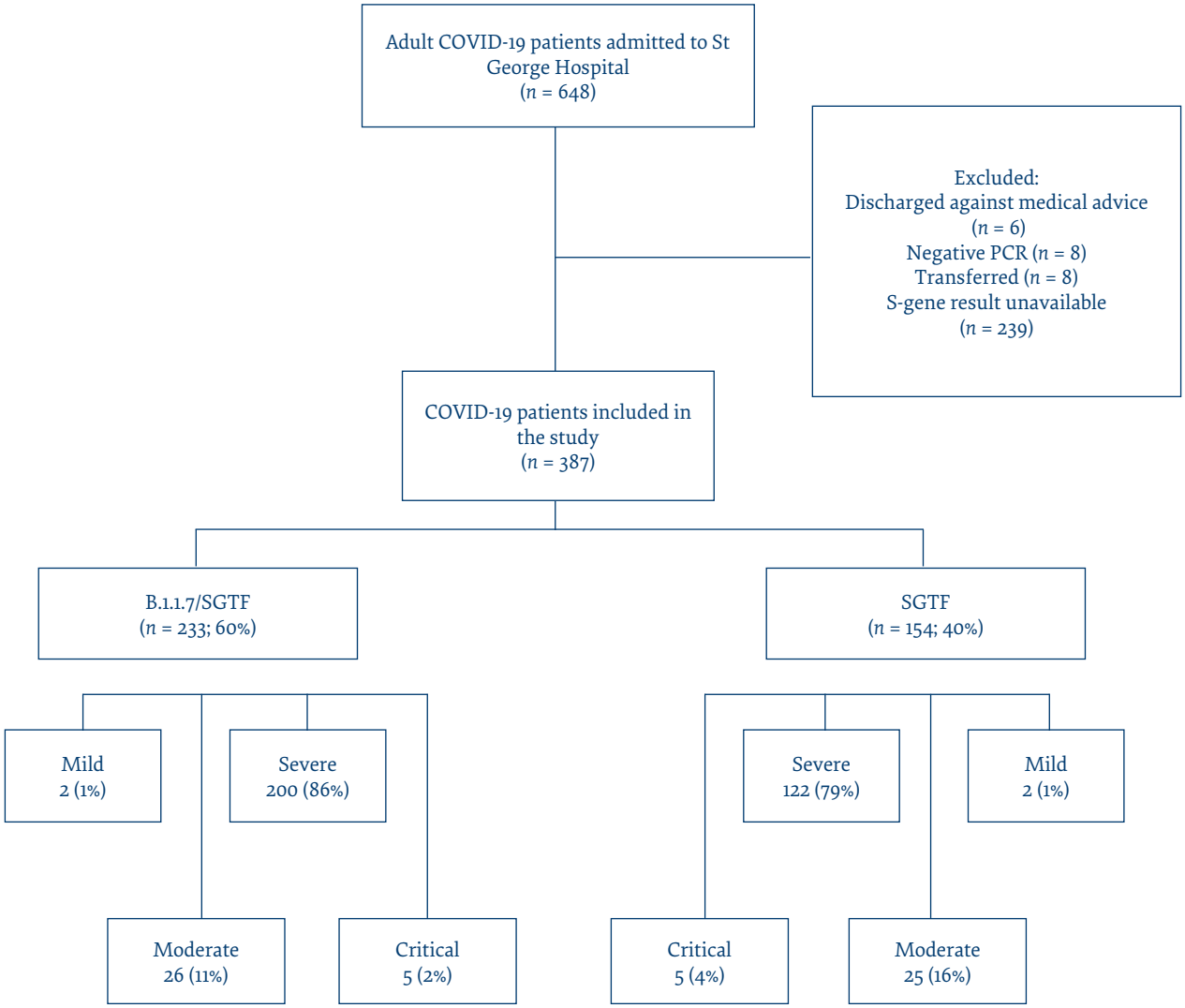
The multivariate logistic regression model was used to determine the risk factors associated with B.1.1.7/SGTF. Clinically relevant variables with a *P*-value < 0.2 in univariate analysis were included in the model. Age was the only continuous variable included, and dummy variables were generated using *SPSS* for categorical variables. To prevent overfitting, the number of outcomes was consistent with the number of independent variables. The Hosmere–Lemeshow and omnibus tests were used to evaluate model fitness. Variables included in the final model were automatically selected by *SPSS* via backward method logistic regression. These included age, smoking, hypertension and cardiovascular disease. Probability values were 2-sided, with statistical significance set at $P < 0.05$. None of the variables included in the study had missing values and there was no patient loss to follow-up.

Results

Patient characteristics

Of the 644 adult COVID-19 patients admitted to Saint George Hospital between December 2020 and February 2021, 387 were confirmed as eligible, included in the analysis and completed their follow-up (Figure 1). The median age of the cohort was 59 years; 66% of the patients were male (Table 1). Most patients had severe COVID-19 (83%), with only 3% having critical illness. Patients admitted to the ICU (26%) spent a median duration of 10 days in the ward. In-hospital mortality was 23%, and a small proportion of the cohort (20%) were administered mechanical ventilation. The proportion of patients aged

Figure 1 Flow chart showing selection of the study participants and SGTF status among adult COVID-19 patients admitted to Saint George Hospital between December 2020 and February 2021



< 65 years was greater in the B.1.1.7/SGTF group [162/233 (70%) vs 74/154 (48%); $P < 0.0001$]. Only non-SGTF patients experienced multi-organ failure [5/154 (4%) vs 0/233 (0%); $P = 0.0096$].

Median age was 65 years (IQR, 55–76) for the non-SGTF patients ($n = 154$) and 56 years (IQR, 47–68) for the B.1.1.7/SGTF group ($n = 233$) ($P < 0.0001$). Among B.1.1.7/SGTF patients, the highest mortality rate (23.5%) was observed in age groups 50–59 and 60–69 years (Figure 2). The 60–69 and 80–89 years age groups had the highest mortality rate (30%) among non-SGTF patients. We found that B.1.1.7/SGTF was significantly associated with a higher mortality rate (43 % vs 19%; $P = 0.0170$) among female patients only.

Incidence of SGTF and its associated clinical features among hospitalized COVID-19 patients

We determined the incidence of B.1.1.7/SGTF at Saint George Hospital between December 2020 and February 2021. Most hospitalized patients who were admitted in December 2020 (93%) were infected with non-SGTF lineages. The incidence of patients infected with non-SGTF decreased to 42% in January 2021 as the B.1.1.7/SGTF was competing for dominance. The B.1.1.7/SGTF lineage constituted the majority of hospitalized cases (88%) that were admitted in February 2021.

To further investigate the difference in clinical features, the COVID-19 symptoms upon admission were documented (Table 2). Decreased level of consciousness was less common in the B.1.1.7/SGTF group (2% vs 6%; $P = 0.013$), while dyspnoea (91% vs 85%; $P = 0.09$) and myalgia/arthralgia (54% vs 44%; $P = 0.06$) were more prevalent than in the non-SGTF group but in neither of these was the difference statistically significant.

Mortality and ICU admission outcomes among hospitalized patients infected with B.1.1.7/SGTF

To explore the impact of SGTF on COVID-19 outcomes, Kaplan-Meier curves were plotted (Figure 3). The survival curves were compared using the Gehan–Breslow–Wilcoxon test ($\chi^2 = 1.203$, $P = 0.2728$). Survival rates were

Table 1 Epidemiological and clinical characteristics of 387 hospitalized COVID-19 patients in Beirut according to the spike gene target failure status, December 2020–February 2021

Characteristic	Total (n = 387)	Non-SGTF (n = 154)	B.1.1.7/SGTF (n = 233)	P-value
Age, years (median, IQR)	59 (48–72)	65 (55–76)	56 (47–68)	< 0.0001
	No. (%)	**No. (%)**	**No. (%)**	
Male sex	254 (66)	95 (62)	159 (68)	0.1840
Age < 65 years	236 (61)	74 (48)	162 (70)	< 0.0001
Smoker	106 (27)	31 (20)	75 (32)	0.0092
Contact with confirmed cases	197 (51)	81 (53)	116 (50)	0.5881
Severity of illness				
Mild	4 (1)	2 (1)	2 (1)	0.6517
Moderate	51 (13)	25 (16)	26 (11)	0.1485
Severe	322 (83)	122 (79)	200 (86)	0.0883
Critical	10 (3)	5 (4)	5 (2)	0.5276
Comorbidities				
Hypertension	187 (48)	87 (56)	100 (43)	0.0089
Diabetes	125 (32)	51 (33)	72 (31)	0.6468
Cardiovascular disease	129 (33)	43 (28)	86 (37)	0.0664
Comorbid conditions[a]				
0	143 (37)	50 (32)	93 (40)	0.1374
1	85 (22)	37 (24)	48 (21)	0.4257
≥ 2	160 (41)	67 (43.5)	93 (40)	0.4824
Chronic immunosuppression	22 (6)	11 (7)	11 (5)	0.3139
Complications				
In-hospital mortality	88 (23)	37 (24)	51 (22)	0.6234
ICU admission	102 (26)	39 (25)	63 (27)	0.7080
Mechanical ventilation	79 (20)	34 (22)	45 (19)	0.5090
Acute respiratory distress syndrome	82 (21)	32 (21)	50 (21)	0.8727
Cardiac arrest	65 (17)	21 (14)	44 (19)	0.1765
Septic shock	65 (17)	23 (15)	42 (18)	0.4260
Nosocomial infection	43 (11)	11 (7)	32 (14)	0.0434
Multi-organ failure	5 (1)	5 (4)	0 (0)	0.0096
Duration of stay in ICU, days (median, IQR)	10 (6–18)	9 (4–18)	11 (6–21)	0.3750

[a]*Comorbid conditions included: diabetes, hypertension, cardiovascular disease, solid or haematologic malignancy, chronic renal failure, liver disease, asthma and chronic obstructive pulmonary disease.*
IQR = interquartile range.
ICU = intensive care unit.

94% at 12 days and 87% at 21 days among the B.1.1.7/SGTF patients compared with 89% and 80% respectively among the non-SGTF patients (Figure 3). The lowest survival rate in the non-SGTF group (76%) was observed at day 36, and that of the B.1.1.7/SGTF group (78%) at day 50. In the first 24 days following hospital admission, the ICU admission rates were similar for the B.1.1.7/SGTF and non-SGTF groups (χ^2 = 0.0259, P = 0.8720).

Pre-infection predictors of the B.1.1.7/SGTF infection

We identified risk factors associated with B.1.1.7/SGTF infection using multivariate analysis (Table 3). The multivariate model fit was assessed using the Hosmere–Lemeshow (test value = 0.852) and omnibus (omnibus test P-value < 0.001) tests. Baseline clinical features that behaved as independent predictors of B.1.1.7/SGTF infection included smoking (OR = 1.698; CI: 1.023–2.819; P = 0.0410), cardiovascular disease (OR = 3.812; CI: 2.215–6.389; P < 0.0001) and hypertension (OR = 0.415; CI: 0.242–0.711; P = 0.0010). The elderly had lower odds of having B.1.1.7/SGTF infection (OR = 0.379; CI: 0.231–0.622; P < 0.0001).

Discussion

The serendipitous detection of the B.1.1.7 lineage by PCR tests with an S gene dropout paved the way for a few studies to explore its associated clinical characteristics in the community *(15–18)* or in hospitalized cohorts

Figure 2 Mortality rate according to age for hospitalized COVID-19 patients (*n* = 387) in Beirut, December 2020–February 2021

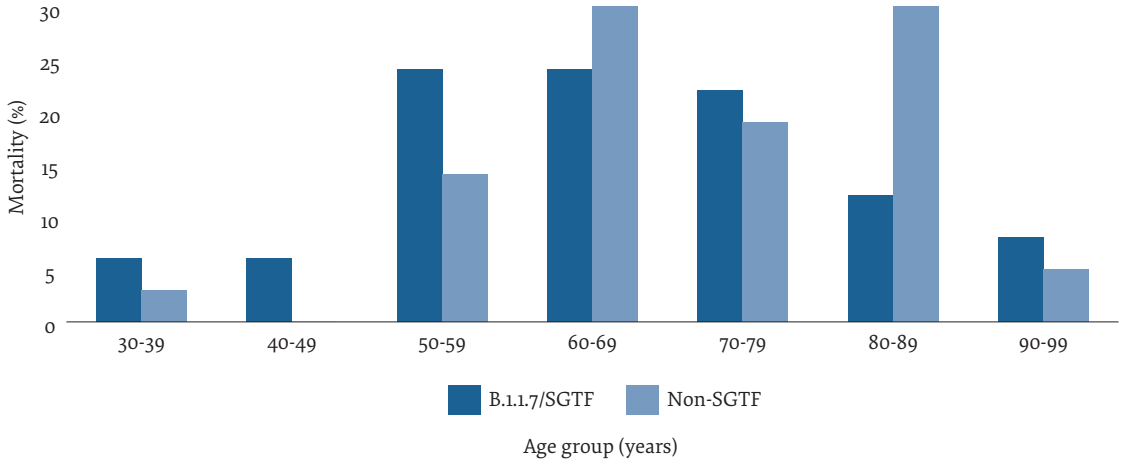
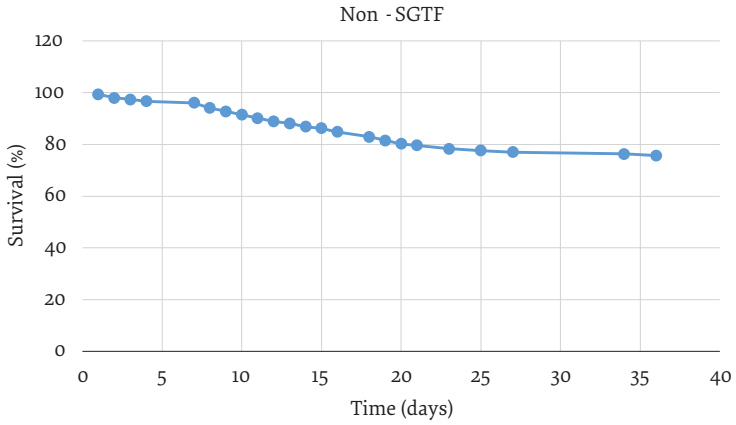
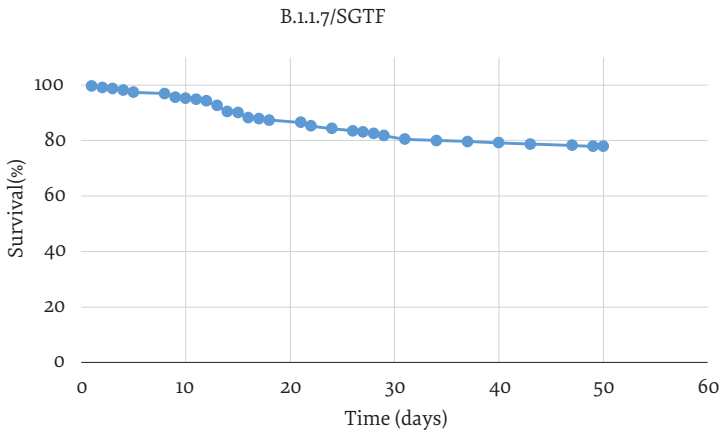


Figure 3 Kaplan-Meier curves showing survival in hospitalized COVID-19 patients (*n* = 387) in Beirut during December 2020–February 2021 according to infection with B.1.1.7/SGTF or non-SGTF lineages (*n* = 387) (SGTF = spike gene target failure); time was plotted as days lapsed from the day of admission (*P* = 0.2728)





(12–14). Our observational cohort study is among the first few to assess the clinical characteristics and outcomes associated with B.1.1.7/SGTF in a hospital. It showed an increased mortality rate among patients infected with B.1.1.7/SGTF, solely in females. Cardiovascular disease and smoking were identified as risk factors for B.1.1.7/SGTF infection.

This study of a hospitalized cohort demonstrated that the overall mortality rate was nonsignificantly different between the B1.1.7/SGTF and the non-SGTF groups. A study in Spain found a similar mortality rate between groups diagnosed with the B.1.1.7/SGTF compared with other variants (12). In a matched case–control study of hospitalized patients, Giles et al. found higher mortality

among B.1.1.7 cases (*22*). However, their result was underpowered by the lack of statistical significance.

Similar to the findings of a study by Stirrup et al. (*13*), this work revealed a significant association between B.1.1.7/SGTF and mortality, but solely among female patients. We did not find a significant association between B.1.1.7/SGTF and COVID-19 severity. Similarly, a recent study in the United Kingdom on hospitalized patients did not find evidence of an association between the B.1.1.7 lineage and severity or death (*14*). Similar to our findings, Veneti et al. found no difference in the ICU admission risk between B.1.1.7 and non-B.1.1.7 among hospitalized cases (*23*).

Hospital statistics may be a reflection of community transmission. Younes et al. started detecting B.1.1.7/SGTF in the Lebanese community from December 2020 (*24*). Another study found that SGTF reached a prevalence of 96.5% in the Lebanese community in February 2021 (*25*). In this study, we demonstrated that the B.1.1.7/SGTF variant displaced other non-SGTF variants at a Lebanese hospital by the end of February 2021.

We determined the overall mortality rate at Saint George Hospital to be 23%, higher than what had been previously reported (19%) (*26*). We explored a panel of clinical characteristics associated with the B.1.1.7/SGTF lineage. Similar to the findings of a previous study carried out in Spain (*12*), the B.1.1.7/SGTF patients in our cohort had a lower median age than non-SGTF patients. Interestingly, our study revealed smoking and CVD to be risk factors associated with B.1.1.7/SGTF infection. Nicotine from smoking has been shown to upregulate ACE2 receptors in pulmonary epithelial cells (*27*). Fagyas et al. showed that ACE2 levels were substantially elevated among heart failure patients, suggesting a role of ACE2 in the pathomechanisms of CVD (*28*). The B.1.1.7 variant has a mutation that increases the binding affinity between the S-protein and ACE2 (*8*), a receptor critical for cell entry. Since the heart can be directly infected by SARS-CoV-2, one may expect increased susceptibility of CVD patients

Table 2 Distribution of COVID-19 patients on admission to a Lebanese hospital according to symptoms and spike gene target failure status, December 2020–February 2021

Symptom	Total (*n* = 387)	Non-SGTF (*n* = 154)	B.1.1.7/SGTF (*n* = 233)	*P*-value
	No. (%)	No. (%)	No. (%)	
Dyspnoea	342 (87)	131 (85)	211 (91)	0.09
Dry cough	297 (76)	118 (77)	179 (77)	0.96
Fever	280 (71)	109 (71)	171 (73)	0.57
Myalgia/arthralgia	193 (49)	68 (44)	125 (54)	0.06
Headache	79 (20)	30 (19)	49 (21)	0.7
Nausea	63 (16)	21 (13)	42 (18)	0.25
Diarrhoea	48 (12)	18 (12)	30 (13)	0.72
Chest pain	34 (9)	14 (9)	20 (9)	0.86
Sore throat	32 (8)	14 (9)	18 (8)	0.63
Productive cough	31 (8)	10 (6)	21 (9)	0.37
Abdominal pain	31 (8)	12 (8)	19 (8)	0.89
Anosmia	16 (4)	6 (4)	10 (4)	0.84
Decreased level of consciousness	14 (3.5)	10 (6)	4 (2)	0.013

Table 3 Predictors of the B.1.1.7/SGTF infection among 387 hospitalized COVID-19 patients in Beirut, December 2020–February 2021

Characteristic	Univariate analysis			Multivariate analysis		
	OR	95% CI	P-value	OR	95% CI	P-value
Cardiovascular disease	1.510	0.971–2.348	0.0664	3.812	2.215–6.389	< 0.0001
Smoking	1.883	1.165–3.045	0.0092	1.698	1.023–2.819	0.0410
Hypertension	0.579	0.383–0.873	0.0089	0.415	0.242–0.711	0.0010
Age ≥ 65 years	0.405	0.265–0.618	< 0.0001	0.379	0.231–0.622	< 0.0001
Male sex	1.334	0.871–2.044	0.1840			
Diabetes	0.903	0.584–1.397	0.6468			
Contact with confirmed cases	0.893	0.594–1.343	0.5881			
Chronic immunosuppression	0.644	0.272–1.525	0.3139			

OR = odds ratio; CI = confidence interval.

to infection with the B.1.1.7/SGTF lineage. Although not statistically significant, we also observed a higher prevalence of cardiac arrest among B.1.1.7/SGTF patients (19% vs 14%; *P* = 0.17). Hypertension was associated with a lower risk for B.1.1.7/SGTF infection in our cohort. It would be interesting to investigate the potential dysregulation of ACE2 in the lungs of hypertensive patients, and the effect of treatment with renin-angiotensin-aldosterone system inhibitors.

One of the limitations of this study is the lack of sequencing experiments, which remain the gold standard for confirming the detection of a variant of concern. Moreover, the analysis would have benefited from a larger cohort size.

This study offers a precise estimation of mortality through an advantageous analytical approach. Some studies measured death within 28 days from diagnosis (*13*,*14*) or followed up patients for only 14 days after the onset of symptoms (*12*). We did not limit our mortality analysis to a specific time. We conducted survival analysis, rather than solely comparing overall mortality rates. This analysis does not include vaccination cases that were unaccounted for. Another strong point of the study is the generalizability of its results to Lebanon, a country with a small area and small population. Moreover, in view of its status as a specialty centre for the pandemic, Saint George Hospital received a substantial number of COVID-19 patients.

Viral mutations can result in advantages in transmissibility but may also alter the clinical characteristics among infected individuals. Omicron (B.1.1.529) was designated by the World Health Organization as a variant of concern on 26 November 2021 (*29*); it is the only lineage that shares the SGTF characteristic with the B.1.1.7. variant. In countries with a low prevalence of the B.1.1.7 variant, SGTF was recommended by WHO as a marker for Omicron.

Conclusion

Epidemiological surveillance is crucial for deciphering viral evolution and monitoring alterations in transmissibility and disease pathology. This study provides insight into the clinical features associated with the alpha variant. Similar studies should be conducted on other variants of concern to track changes in viral pathogenesis. Our study shows that B.1.1.7/SGTF was associated with higher mortality but among female patients only. It shows that smoking and CVD were associated with increased odds of B.1.1.7/SGTF infection. On the other hand, hypertension was associated with decreased odds of B.1.1.7/SGTF infection while B.1.1.7/SGTF was associated with a significantly lower median age.

Acknowledgement

The authors would like to thank all the staff at Saint George Hospital for their cooperation.

Funding: None

Competing interests: None declared.

Étude de cohorte observationnelle des résultats cliniques associés au SGTF lié au B.1.1.7 chez des patients COVID-19 hospitalisés au Liban

Résumé

Contexte : Le variant B.1.1.7 SARS-CoV-2 entraîne l'absence de détection du gène S (SGTF) dans les tests de réaction en chaîne par polymérase après transcription quantitative inverse (RT-PCR). Peu d'études ont été publiées sur l'impact clinique du SGTF/B 1.1.7.

Objectifs : Évaluer l'incidence du SGTF/B 1.1.7 et ses caractéristiques cliniques associées chez les patients hospitalisés atteints de COVID-19.

Méthodes : La présente étude observationnelle de cohorte monocentrique a été menée entre décembre 2020 et février 2021 auprès de 387 patients hospitalisés atteints de COVID-19. La méthode de Kaplan-Meier a été utilisée pour l'analyse de survie et la régression logistique afin de déterminer les facteurs de risque associés au SGTF/B.1.1.7.

Résultats : En février 2021, le SGTF/B.1.1.7 (88 %) a dominé les résultats de la PCR du SARS-CoV-2 dans un hôpital libanais. Sur les 387 patients éligibles atteints de COVID-19 confirmés pour le SARS-CoV-2 par RT-PCR, 154 (40 %) étaient négatifs pour le SGTF et 233 (60 %) étaient positifs pour le SGTF/B 1.1.7 ; cela était associé à un taux de mortalité plus élevé chez les femmes [22/51 (43 %) contre 7/37 (19 %) ; p = 0,0170]. Parmi les patients du groupe SGTF/B 1.1.7 la plupart étaient âgés de 65 ans et plus [162/233 (70 %) *contre* 74/154 (48 %) ; p < 0,0001]. Les facteurs prédictifs indépendants de l'infection par le B.1.1.7/SGTF étaient l'hypertension (OR = 0,415 ; IC : 0,242-0,711 ; p = 0,0010), le fait d'être âgé de 65 ans et plus (OR = 0,379 ; IC : 0,231-0,622 ; p < 0,0001), le tabagisme (OR = 1,698 ; IC : 1,023-2,819 ; p = 0,0410) et les maladies cardiovasculaires (OR = 3,812 ; IC : 2,215-6,389 ; p < 0,0001). Seuls les patients négatifs pour le SGTF présentaient une défaillance multiviscérale [5/154 (4 %) *contre* 0/233 (0 %) ; p = 0,0096].

Conclusion : Il y avait une différence claire entre les caractéristiques cliniques associées aux lignées B.1.1.7/SGTF et celles ne présentant pas de SGTF. Le suivi de l'évolution virale et de son impact clinique est essentiel à la compréhension et à la gestion de la pandémie de COVID-19.

دراسة أترابية رصدية للنتائج السريرية المرتبطة بزيادة فشل الجين المستهدف الناجم عن المتحور B.1.1.7 في صفوف المصابين بكوفيد-19 الذين تلقوا الرعاية في المستشفيات في لبنان

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الخلاصة

الخلفية: يتسبب المتحور B.1.1.7 لفيروس كورونا-سارس-2 في زيادة فشل الجين المستهدف في مقايسات التنسُّخ العكسي لتفاعل البوليميراز المتسلسل الكمي. وقد نُشر عدد قليل من الدراسات عن الأثر السريري لزيادة فشل الجين المستهدف الناجم عن هذا المتحور.

الأهداف: هدفت هذه الدراسة إلى تقييم معدل حدوث زيادة فشل الجين المستهدف الناجم عن المتحور B.1.1.7 والخصائص السريرية المرتبطة به في صفوف المصابين بكوفيد-19 الذين يتلقون الرعاية في المستشفى.

طرق البحث: أُجريت هذه الدراسة الأترابية الرصدية الأحادية المركز في المدة ما بين ديسمبر/ كانون الأول 2020 وفبراير/ شباط 2021، وشملت 387 مريضًا من مرضى كوفيد-19 الذين تلقوا الرعاية في المستشفى. واستُخدم أسلوب كابلان-ماير لتحليل البقاء على قيد الحياة، وأسلوب الانحدار اللوجستي لتحديد عوامل الخطر المرتبطة بزيادة فشل الجين المستهدف الناجم عن المتحور B.1.1.7.

النتائج: بحلول فبراير/ شباط 2021، سيطرت زيادة فشل الجين المستهدف الناجم عن المتحور B.1.1.7 على نتائج اختبار تفاعل البوليميراز المتسلسل لفيروس كورونا-سارس-2 (88٪) في أحد مستشفيات لبنان. ومن بين مرضى كوفيد-19 المؤهلين، البالغ عددهم 387 مريضًا، الذين تأكدت إصابتهم بواسطة التناسخ العكسي لتفاعل البوليميراز المتسلسل لفيروس كورونا-سارس-2، لم يتعرض 154 مريضًا (40٪) لزيادة فشل الجين المستهدف، وتعرَّض 233 مريضًا (60٪) لزيادة فشل الجين المستهدف الناجم عن المتحور B.1.1.7؛ وارتبط ذلك بمعدل وفيات أعلى في صفوف النساء المريضات [51/ 22 (43٪) مقابل 37/ 7 (19٪)؛ القيمة الاحتمالية = 0.0170]. وكان معظم المرضى ضمن الفئة التي تعرَّضت لزيادة فشل الجين المستهدف الناجم عن المتحور B.1.1.7 في سن 65 عامًا فأكثر [233/ 162 (70٪) مقابل 154/ 74 (48٪)؛ القيمة الاحتمالية < 0.0001]. وتمثَّلت المنبئات المستقلة للإصابة بزيادة فشل الجين المستهدف الناجم عن المتحور B.1.1.7 في ارتفاع ضغط الدم (نسبة الأرجحية = 0.415؛ فاصل ثقة: 0.242–0.711؛ القيمة الاحتمالية = 0.0010)، وبلوغ سن 65 عامًا فأكثر (نسبة الأرجحية = 0.379؛ فاصل ثقة: 0.231–0.622؛ القيمة الاحتمالية < 0.0001)، والتدخين (نسبة الأرجحية = 1.698؛ فاصل ثقة: 1.023–2.819؛ القيمة الاحتمالية = 0.0410)، وأمراض القلب والأوعية الدموية (نسبة الأرجحية = 3.812؛ فاصل ثقة: 2.215–6.389؛ القيمة الاحتمالية < 0.0001). وكان المرضى غير المصابين بزيادة فشل الجين المستهدف وحدهم يعانون فشلَ أعضاء متعددة [154/ 5 (4٪) مقابل 233/ 0 (0٪)؛ القيمة الاحتمالية = 0.0096].

الاستنتاجات: كان هناك فرق واضح بين المظاهر السريرية الناجمة عن السلالات المرتبطة بزيادة فشل الجين المستهدف الناجم عن المتحور B.1.1.7 والسلالات غير المرتبطة بزيادة فشل الجين المستهدف. ويُعَدُّ تتبُّع تطور الفيروس وأثره السريري أمرًا بالغ الأهمية لفهم جائحة كوفيد-19 وتدبير المرض علاجيًّا بطريقة صحيحة.

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